Published in final edited form as:

Behav Genet. 2010 November ; 40(6): 776–783. doi:10.1007/s10519-010-9373-x.

Analyzing Intra-person Variation: Hybridizing the ACE Model with P-Technique Factor Analysis and the Idiographic Filter

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Abstract

Integrating idiographic and nomothetic approaches to the study of behavior has met with success via the idiographic filter (IF) which separates irrelevant inter-individual differences from relevant inter-individual similarities at the level of construct measurement in order to facilitate drawing conclusions regarding nomothetic relationships among the constructs. We propose an integration of the IF and the ACE behavior genetics models through the use of P-technique factor analysis and its dynamic factor analysis extensions and examine how it can strengthen the modeling of genetic and environmental effects in behavioral data representing intra-person variation, change, and process.

Keywords

Intraindividual variability; Process; Idiographic filter; ACE model

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Empiricism works well in the physical sciences. In behavioral science it means well but apparently works more slowly, judging from the relative levels of accomplishment in producing important lawful relations in the two kinds of science. Perhaps one of the chief reasons for difficulties in behavioral science is that there are layers of unobservable events residing behind observable human behavior and the environmental contexts in which the behavior plays out that are apparently without counterpart in the physical sciences. This is not to say that unobservable events are absent in physical science phenomena—far from it. However, driving the *human* behavioral act are intentions, motives, aspirations, unconscious components, etc., (see, e.g., Ford 1987), whereas a bar of iron just lies still and oxidizes away with neither remorse nor concern about its future. It did not have to learn how to oxidize nor, as time passes, will it forget how to do it. It just “happens,” according to well-understood laws.

Behavioral scientists attempt to cope with the subjective, unobservable layers with a variety of methods (including neglect) which, of necessity, involve various forms of inference regarding theoretically useful hypothetical constructs. Although there is not inter-subjective testability of all the mental events accompanying the overt behavioral act there can be inter-subjective testability of overt behaviors of people, including some measurable brain events (e.g., via fMRI). But such inter-subjectively testable behaviors are only a part of the

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behavioral act. There still remain hypothesized but not observable internal events that appear to be peculiar to at least some life forms.

Unobservable constructs and lawful relations among them are key features of theory but unless these yield empirically testable propositions regarding related observable measures theory building does not advance. In behavioral science, the limited access to internal events, states, etc., profoundly influences the measurement operations we perform. Concerns run from very practical matters such as the reliability of the measures to more abstract ones including how well given observable measures reflect the unobservable constructs they are supposed to represent. Trying to do some mapping of these inaccessible regions is a major part of theory construction but it is an activity that is obviously fraught with peril.

Developing strong linkages between observable and unobservable events in order to pierce the veil obscuring the latter has long been a major concern of psychological measurement, or psychometrics. Multivariate measurement schemes hold an important place in the psychometric literature because of their emphasis on and capacity for representing latent variables through the use of batteries of manifest variables. Baltes and Nesselroade (1973), for example, identified three primary reasons why measurement schemes ought to be multivariate in nature when studying developmental processes. Subsequently, Nesselroade and Ford (1987) elaborated these to emphasize their pertinence to dynamical systems representations, resulting in the following four-element rationale favoring multivariate measurement schemes:

1. Any dependent variable (or consequent) is potentially a function of multiple determinants.
2. Any determinant or antecedent has potentially multiple consequents.
3. Any determinant or antecedent may also be considered a consequent of other determinants or antecedents, and any consequent may also be considered a determinant or antecedent of some other consequents.
4. The study of multiple antecedent-consequent relationships provides a useful model for the organization of complex systems.

With the structural equation modeling (SEM) movement came improvements in ways to conceptualize and implement the measurement of latent variables and the ability to evaluate how well this is being done that elevated this general multivariate approach to the representation of latent variables or constructs to a level of sophistication that supported its introduction to a variety of other areas of quantitative modeling including behavior genetics (Martin and Eaves 1977; McArdle and Goldsmith 1990). We will return to this topic subsequently but first will lay some more groundwork for adapting the measurement of latent variables for use in a variety of modeling efforts.

P-Technique Factor Analysis and the Idiographic Filter

One of the most elegant methods for accomplishing the measurement of unobserved, latent variables that has been devised by behavioral scientists is rooted in the common factor analysis model and rests heavily on the concept of factorial invariance (Meredith 1964, 1993; Meredith and Horn 2001; Millsap and Meredith 2007; Thurstone 1947). Central in this regard are the factor loadings which are, by definition of the factor model, the linkages between observables (manifest variables) and unobservables (factors or latent variables). When factor loadings are demonstrably invariant from one data sample to another the measurement implications are profound. For instance, factor loadings that remain invariant from one set of measurements to a later, repeated set of measurements make it plausible to argue that, if change has been observed, it is the person’s measurement on the underlying

factor and not which attribute of the person being measured that has changed, thus providing a convincing basis for calculating and interpreting change scores on the observed variables and/or the factors (e.g., Nesselroade 1970).

Were it so simple. Factor loadings are both a blessing and a curse. They are a blessing under conditions of invariance because they provide critical information regarding the pathways between the observed and the unobserved and support the kinds of calculations mentioned above. But, they can be a curse when invariance is lacking because there are several possible explanations for why, some of which are important to a given purpose and some of which are not. For example, if invariance fails to describe one's data, is it because the relations are indeed not invariant or is it because of the way the observables are being conceptualized and measured?

Nesselroade et al. (2007) proposed using P-technique factor analysis—factoring multivariate time series based on the single case—as an idiographic filter (IF) for integrating idiographic and nomothetic approaches to the study of behavior with an emphasis on measurement properties. They argued that, in certain circumstances and for a variety of reasons unrelated to the actual measurement of constructs, manifest or observed variables that are ostensibly the same may actually not represent the same qualities from one person to another. Such circumstances negate the usual conceptions of measurement comparisons and raise questions concerning the concept of invariance. Therefore, some flexibility in the linkages between manifest and latent variables should be tolerated from one individual to another and, provided a rigorous version of invariance could be demonstrated at the latent level, such a model can be fitted and evaluated for its fit to data. To illustrate how this thinking might be used to enhance behavior genetics modeling, we first provide a brief summary of P-technique factor analysis and then examine the IF in more detail.

P-technique factor analysis was introduced over a half-century ago (Cattell et al. 1947; Cattell 1963) and continues to be examined and used in various contexts (Browne and Nesselroade 2005; Molenaar and Nesselroade 2009; Rausch 2009). It involves the application of the common factor model to multivariate, repeated measurements of one individual obtained over a substantial number of occasions—a multivariate time series. Thus, P-technique data carry information concerning one individual so variance in the scores on a given observable indicates intraindividual fluctuations in performance or other functioning. Assuming that the attributes being measured are the same attributes across the entire time series, the patterns of covariation over time can be decomposed into factors of intraindividual variation. Although the results of a given analysis are unique to one person, the results from multiple cases can be examined for similarities as well as differences among participants.

Cattell's purpose in introducing P-technique factor analysis was not so much to identify different constructs for each individual as it was to identify individualized versions of the same general constructs. Ever the systematist, Cattell's arguments regarding the ultimate similarities of R- and P-technique factors (see, e.g., Cattell 1963) suggest that he did not have in mind the elaboration of idiosyncratic traits per se, but, rather, taking account of the idiosyncratic expression of traits found generally in the population. State anxiety is a prime example of the kind of dimension Cattell pursued via the use of multivariate methods (Cattell and Scheier 1961). He regarded state anxiety to be a general attribute, albeit one of within person variation, and contributed to the development of self-report measures for it, letting P-technique studies inform the work just as did R- and dR-technique (group designs) research.

In the ensuing years since the introduction of P-technique factor analysis, many authors argued for the value of individual-level analysis outcomes as a basis for conducting more informed aggregation of information over multiple individuals (Lebo and Nesselroade 1978; Molenaar 2004; Nesselroade and Ford 1985; Zevon and Tellegen 1982) and suggested that P-technique factor analysis was one basis for accomplishing this. Other writers (e.g., Anderson 1963; Holtzman 1963) argued that P-technique was flawed for both statistical and conceptual reasons. A series of important discussions further explicated the shortcomings of P-technique and presented various solutions for dealing with them (Browne and Nesselroade 2005; Cattell 1963; Molenaar 1985).

Procedures generally referred to as *dynamic factor analysis* (DFA) that explicitly model lagged relationships between the factors and observed variables either directly or indirectly, have been developed and explored as improvements on the original P-technique model (see e.g., Browne and Nesselroade 2005; Molenaar 1985; Nesselroade et al. 2002). Recent work (Molenaar and Nesselroade 2009) indicates that the somewhat maligned P-technique model continues to be resilient enough to provide important guidance in modeling multivariate time series. P-technique's appeal [for Bereiter (1963) it is "the logical technique for studying the interdependencies of measures" (p.15)] coupled with its durability and noted strengths suggest that re-evaluating its potential for contributing to the study of the individual from a broad perspective would not be amiss.

In articulating a rationale for applying the IF, Nesselroade et al. (2007) "structured" the matter in terms of preventing idiosyncratic features of individual behavior at the measurement level from hiding what is common in behavior across individuals (nomothetic relationships) at the construct level. The essential idea of the IF is that one can seemingly violate the traditional concept of standardized measurement by building P-technique factor analytic representations that are somewhat uniquely tailored to the individual while retaining the concept of invariance at a higher level of abstraction in order to identify the same constructs (latent variables) underlying the behavior of different individuals. Of course, the meaning of *same* is what is really at stake here. Nesselroade et al. (2007) offered one solution to defining *same* for different individuals by employing a P-technique factor analysis approach and allowing idiosyncratic patterns of factor loadings at the first-order level while constraining the factor loadings at more abstract levels (e.g., the second order) to be invariant in the traditional sense. Thus, the first order factors were used to filter out idiosyncrasies that are irrelevant to the interrelations of those first order factors, allowing the interrelations (factor intercorrelations) to be invariant across people. Invariant first order factor intercorrelations, in turn, defined invariant second-order factors.

The IF is illustrated in Fig. 1 for two hypothetical P-technique participants who have been repeatedly administered a battery of tests (a through l) that are modeled by three first-order factors (F_1, F_2, and F_3). Note that even though there is some idiosyncrasy in the primary factor loading patterns, the factor intercorrelations are the same for the participants thus indicating that a second order factor solution would be invariant, in the traditional sense, over the participants. Projecting the observed variables directly onto the second-order factors by a Schmidt–Leiman or Cattell–White transformation (Loehlin 1998) gives for each participant an individually tailored (filtered) representation of what can be argued to be the same second-order factor (general construct).

Nesselroade et al. (2007) illustrated their points with self-reported affect measures collected in a replicated P-technique factor analysis design, but there are other content domains for which the measurement of constructs seems to be just as vulnerable to being "sabotaged" by idiosyncratic features of behavior. For example, the general ideas associated with the IF, if not the label, have been amply discussed in the psychophysiological literature (e.g.,

Friedman and Santucci 2003; Stemmler 1992) under response specificity in the autonomic nervous system. These concerns reflect an awareness of the way idiosyncratic learning and conditioning histories “tune” the individual’s patterns of response to stimuli. As an individual develops, the “hard wiring” of physiological responses by Mother Nature becomes overlaid with the effects of learning and conditioning, for example, to the extent that a given observable physiological variable may reflect quite different patterns of relations with unobservables in different people—so much so that it makes little sense to presume that just because one has used the same measurement procedure on different people (e.g., a sphygmomanometer to measure blood pressure in the brachial artery while the individual is in a sitting position) that the measurements can be meaningfully combined into means, variances, etc., or used as a general indicator of underlying processes.

The dynamic factor models mentioned earlier provide a promising way to conceptualize latent entities that embody important process characteristics. Aided by the multivariate measurement orientation (Baltes and Nesselroade 1973; Cattell 1966; Nesselroade and Ford 1987) described earlier, dynamic factor models can play for processes a role similar to that played by P-technique for latent variables. Dynamic factor models, for example, incorporate systematic continuities (i.e., the effects of earlier states on later ones), either among factors or between factors and manifest variables (see, e.g., Nesselroade et al. 2002). Coupling this idea with the IF provides a means to allow for a common underlying process (nomothetic relations) to differ in the actual physical manifestations (indicators or manifest variables) from individual to individual (idiographic relations).

With the modeling of intraindividual variability via the IF and P-technique and its derivatives as a way to capture processes of change and assign scores to individuals that describe the change characteristics, we now turn to the examination of some relevant ideas through the lens of behavior genetics modeling. Our proposed modeling of intraindividual variability via behavior genetics models extends a possibility briefly discussed two decades ago by Plomin and Nesselroade (1990).

Behavior Genetics Modeling

Traditional approaches to disentangling genetic and environmental effects, regardless of how sophisticated the quantitative modeling involved may be, hinge on measurements of some phenotypic variable of interest. A phenotype can be any characteristic—an observed score on a rather easily measured physical characteristic such as height or weight or an estimated score on an underlying, latent variable that is not directly observable such as anxiety, life satisfaction, or depression. It can be an independent variable in some relation of interest, or a dependent variable, or a correlate. A phenotype can be a regression weight in individualized growth curves, some other system parameter, or something as abstract as the conductivity tensor in a wave model for the depolarization wave of the heart.

Can the IF ideas be usefully applied to the measurement of phenotypes for behavior genetic modeling? Because a phenotype can be an individual’s factor (latent variable) score, for example, we believe there is great potential for using some version of the IF in the context of behavior genetics modeling. We are proposing this application for two primary reasons. First, the IF idea was initially articulated in the context of P-technique factor analysis which focuses on individual-level process and change manifestations rather than static attributes of the individual.[1] We believe firmly that this is the direction in which behavioral research is (and should be) heading. Further, the extensions of the basic P-technique model identified as

[1]P-technique and dynamic factor modeling are focused on phenotypic systems (not just phenotypic variables) and are approaches that match well with G. E. McClearn’s long and productive career involving systems approaches in behavior genetics.

dynamic factor models (e.g., Browne and Nesselroade 2005;Browne and Zhang 2005;Molenaar 1985) provide tools for developing phenotypic variables that reflect key features of process such as auto- and cross-regression coefficients at both the manifest and latent levels. Second, the IF provides a basis for "cleaning up" the measurements of concepts at the individual level by reducing, if not eliminating, idiosyncratic behavior that intrudes on the measurement process but is not directly reflective of the attribute one is attempting to measure. For behavior genetics modeling, the IF has the potential for developing phenotypes that both reflect aspects of change processes and are "tailored" to the individual members of twin pairs for the purpose of minimizing irrelevant idiosyncrasy. Thus, the IF opens the door to a number of possibilities such as more idiosyncratic measurement of the two members of a twin pair not previously entertained in behavior genetic modeling.

As we have described the IF, one does not represent it with a single factor score per subject, but a time series of such factor scores—the estimated latent factor time series for each subject. The estimated factor series can be treated like other time series (e.g., EEG) in twin studies and many possible kinds of statistics can be derived per subject to serve as the phenotype of interest. For instance the auto-regressive beta coefficients, the process noise, the cross-lagged correlations, anything we deem interesting can serve as the phenotype in a quantitative genetic analysis.

Clearly, it is important in quantitative genetic modeling to define the phenotypic values of the participants at the most appropriate level for one's concerns. We believe that multivariate time series data provide a useful set of insights into some kinds of processes and propose to model them with some variant of P-technique and the IF in order to lessen, if not eliminate, idiosyncrasy of the measured properties that will be used as the phenotype for further analysis. Using the IF is intended to emphasize relations at the latent level more so than those at the manifest level but, as noted earlier, that does not prevent one from extracting phenotypic information of interest from the idiographically filtered constructs.

To illustrate the ideas in more detail, we reference the commonly used ACE model (Martin and Eaves 1977) which is based on the general factor analytic model with separate factors representing (1) additive genetic variance (A), (2) shared environmental influences (C), and (3) non-shared environmental influences (E). An alternative model that is closely linked to the common factor model was called the psychometrical genetics model by McArdle and Goldsmith (1990). A joint path diagram for these two models is given in Fig. 2. Either of these models suffices to indicate the essential nature of the approach we will propose—to link the IF with the ACE behavior genetics model in order to improve the specification and measurement of phenotypic variables for quantitative behavior genetics research. We now examine that possibility more closely.

Integrating the Idiographic Filter with the ACE Model

The IF as identified in the context of P-technique modeling can be integrated with ACE behavior genetics modeling in a straightforward way to get at change processes. An obvious series of steps includes:

1. Use P-technique, and/or its dynamic factor analysis successors with the IF to identify and represent processes of interest. Such analyses can be conducted on twins, adoptees, or other populations of behavior genetic interest.
2. Calculate/estimate values of interest (e.g., factor scores, auto-regressive parameters, process noise parameters, cross-lagged correlations) for each member of a twin pair.

3. Use the values as phenotypic expressions to be analyzed by models such as variations on the ACE behavior genetics model in order to better understand the nature of process and change.

Combining the IF with the ACE behavior genetics model does raise some issues of feasibility. Typically, for example, P-technique factor analysis and its dynamic factor analysis extensions involve intensive assessments of a relatively small number of individuals whereas traditional quantitative behavior genetics modeling usually involves assessments of a large number of individuals on only a few (often just one) occasions of measurement. Cattell (1963), for example, mentions 100 occasions of measurement as a target for collecting P-technique data. P-technique involves an implicit assumption that, for a give participant, the measures do not change in meaning over time. Behavior genetics studies often involve more than 100 pairs of twins in various configurations. For the resources of most researchers, combining such numbers of occasions and twin pairs is prohibitive unless one is measuring via some kind of physiological recording such as EEG. But, we hasten to add that because the key concern is constructing a phenotype of interest one may be content to measure and apply idiographic filtering to data representing substantially smaller numbers of occasions of measurement than, say, 100. The essential key is to have sufficient numbers of occasions that one has meaningful phenotypic variables to analyze via the application of quantitative models.

Using P-technique and some version of the IF to help define phenotypic “fodder” for the ACE models can accomplish two goals: (1) strengthening the modeling of genetic and environmental effects at the construct level by “cleaning up” the quantitative representation of the constructs and (2) by using P-technique factor analysis or its dynamic factor model extensions illustrating an approach to focusing on features of process rather than static attributes.

Because the basic objective of using the IF is to account for idiographic features of behavior that are conflated with the attributes that one is trying to measure, the IF has implications for measuring constructs both within and between families. For example, nuances of language usage may prevail both within and between families to the extent that each individual in a twin pair has a unique history of experience, learning, conditioning, etc., the effects of which on the measurement of constructs can be reduced or perhaps minimized by the IF. Even for twins reared together, for instance, some of the apparent phenotypic differences between them that are usually ascribed to the construct may be due to idiosyncrasies impacting measurement that ought not be part of the ACE modeling procedures. The result of this conflation is that measures of a given construct cannot be relied on to give an accurate picture of the construct from one person to another. The use of the IF can alter this situation, the extent to which remains to be determined.

Molenaar’s iFACE Model

There are two very different approaches to applying the methods of quantitative behavior genetics modeling to intraindividual variability that we wish to distinguish from each other. The one already discussed involves creating an idiographically filtered phenotype of interest and applying traditional quantitative behavior genetics modeling to it. Given that one can “score” participants on an idiographically filtered target variable (phenotype) of interest, any remaining procedural matters are the typical ones of quantitative behavior genetics analysis. A second approach, although it also involves applying behavior genetics modeling to intraindividual rather than interindividual variability, is more radical in nature. Molenaar (2010) developed it and dubbed it the iFACE model because it combines a version of idiographic filtering (iF) with ACE modeling. These two applications are very different in both theory and practice. The first, as mentioned, is essentially “business as usual” from a

quantitative behavior genetics analysis standpoint but the applications are to phenotypes that are constructed from repeated measurements of the participants. The second, the rationale for which rests heavily on the ergodicity arguments that question the capacity of between person variation to inform us regarding within person variation, is an innovative departure from the familiar group-based analyses that feature the decomposition of interindividual differences information to one that emphasizes the analysis of intraindividual variation.

Elsewhere, Molenaar (2010) has argued that, in addition to genes and environment, developmental processes contribute another source of between persons variation at the phenotypic level. He added, however, that developmental processes generally ought to be measured and analyzed at the intraindividual level. Molenaar developed the iFACE model to allow individual level decomposition of phenotypic variables into genetic, environmental, and developmental (process) contributions. With the explanatory as well as the measurement focus on intraindividual variation (e.g., processes) rather than interindividual differences, emphases and concerns other than the usual ones prevail. For example, Molenaar (2010) presented an illustrative simulation based on iFACE modeling applied to a single DZ twin pair and demonstrated how heritability coefficients can be estimated separately for the different members of a twin pair and thus may differ in value for members of the same twin pair.

Emphasizing intraindividual variability is a fundamentally different way of thinking about quantitative behavior genetic modeling but we believe that the arguments favoring analyzing intraindividual variability when one’s overall research focus is on processes rather than static traits are quite compelling. As illustrated by Nesselroade and Molenaar (2010), for example, when one is emphasizing intraindividual variability, such traditionally important concerns as prediction and generalizability take on a very different cast compared to that of an interindividual variability perspective, but the concerns remain highly germane and practically solvable. We believe this general logic can (and should) be extended to the further development and applications of the tools of quantitative behavior genetics methodology.

Discussion

Shifting the focus of behavioral research away from static attributes toward change processes is an important step in the development of our discipline (West 1985). On the positive side, a variety of promising methods and techniques are becoming available for moving beyond the measurement of static concepts to focus on process and change. We believe that researchers are correctly trying to extend this line of reasoning to other areas of behavioral science, including behavior genetics research. One of the limiting factors has to do with how well we can measure the kinds of phenotypic variables that will help advance the study of change and process. It is our contention that a clearer focus on the individual is a key part of this effort (Molenaar 2004; Nesselroade 2010) and we have explored how to accomplish this both within a traditional quantitative behavior genetics approach and via the iFACE model. In that vein, it seems to us that promising alternatives to traditional invariance conceptions that might enable one to disentangle interfering idiosyncratic behavior from construct measurement need to be tried. Such tools can be used to measure behavioral phenotypes bearing on the study of process for further analysis by the methods of behavior genetics.

We have made the point in several ways that modeling at the level of latent variables is an asset in behavioral research. Multivariate measurement schemes have provided a sound avenue for such modeling for over a century. In an effort to improve on the way we measure latent variables, we have discussed the IF as a means for “cleaning up” the representation of

latent variables in general. More to the point for the present chapter, we believe that a focus on change processes via individual variability as modeled by P-technique factor analysis promises to yield important phenotypic variables for behavior genetics analysis. Such analyses can give us much greater insight into behavioral mechanisms at the individual level and combining P-technique factor analysis and the IF with the ACE behavior genetics models raises a number of interesting possibilities for strengthening our efforts better to understand behavioral data.

Implementing the IF approach to measurement opens a number of avenues to a firmer understanding of various change mechanisms. On the one hand, if one minimizes the strictures of standardized measurement and assesses a given construct more appropriately for each member of the twin pair, they might appear to be more, rather than less similar. On the other hand, however, more individually sensitive measurement of constructs may show that members of twin pairs are even less alike than has been thought. It seems to us that this is an empirical question begging for the kind of answer that can be given by applying novel approaches to the measurement of phenotypes.

Although the necessary information and techniques for intervening at the level of processes are mainly lacking, this is surely an important direction in which to be heading. The adaptations we have suggested offer means by which we can move in that direction. The future of behavioral science rests on the development and application of process-oriented, dynamic conceptions of behavioral attributes manifested by individuals and the development of methods by which this can be accomplished are receiving more and more attention. It is an exciting time, but not so for the faint-hearted.

Acknowledgments

This work was supported by R21 Grant AG034284-01 from the National Institute on Aging, National Institutes of Health (USA) and National Science Foundation Grant 0852147.

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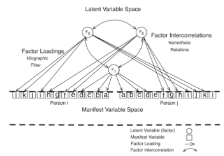

Fig. 1.

Schematic illustration of the idiographic filter depicting 3-factor models for two P-technique participants measured on 12 variables

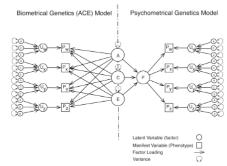

Fig. 2.
Path diagram for the biometrical genetics (ACE) model (Martin and Eaves 1977) and psychometrical genetics model (McArdle and Goldsmith 1990). The two models are separated by the vertical centerline. Both models include the central factors A, C, and E